

Input file Fbhl4790FL.seq; Output file 14790.trans
Sequence length 5525

SEQUENCE ID NO:2

SEQUENCE ID NO:1

TCGCCCCACGCGTCCGACCGCCGCCAGGCAAGGCCGCCCTGCCTTGGGCGCAGCGCTGCC	M A G G	4
R G A P G R G R D E P P E S Y P Q R Q D	ATG GCT GGG GGC	12
CGT GGG GCC CCC GGG CGC GGC CGG GAC GAG CCT CCG GAG AGC TAC CCG CAA CGA CAG GAC		24
H E L Q A L E A I Y G A D F Q D L R P D		72
CAC GAG CTA CAG GCC CTG GAG GCC ATC TAC GGC GCG GAC TTC CAA GAC CTG CGG CCG GAC		44
A C G P V K E P P E I N L V L Y P Q G L		132
GCT TGC GGA CCG GTC AAA GAG CCC CCT GAA ATC AAT TTA GTT TTG TAC CCT CAA GGC CTA		64
T G E E V Y V K V D L R V K C P P T Y P		192
ACT GGT GAA GAA GTA TAT GTA AAA GTG GAT TTG AGG GTT AAA TGC CCA CCT ACC TAT CCA		84
D V V P E I E L K N A K G L S N E S V N		252
GAT GTA GTT CCT GAA ATA GAG TTA AAA AAT GCC AAA GGT CTA TCA AAT GAA AGT GTC AAT		104
L L K S R L E E L A K K H C G E V M I F		312
TTG TTA AAA TCT CGC CTA GAA GAA CTG GCC AAG AAA CAC TGT GGG GAG GTG ATG ATC TTT		124
E L A Y H V Q S F L S E H N K P P P K S		372
GAA CTG GCT TAC CAC GTG CAG TCA TTT CTC AGC GAG CAT AAC AAG CCC CCT CCC AAG TCT		144
F H E E M L E R R A Q E E Q Q R L L E A		432
TTT CAT GAA GAA ATG CTG GAA AGG CGG GCT CAG GAG GAG CAG CAG AGG CTG TTG GAG GCC		164
K R K E E Q E Q R E I L H E I Q R R K E		492
AAG CGG AAA GAA GAG CAG GAG CAA CGT GAA ATC CTG CAT GAG ATT CAG AGA AGG AAA GAA		184
E I K E E K K R K E M A K Q E R L E I A		552
CGAG ATA AAA GAA GAG AAA AAA AGG AAA GAA ATG GCT AAG CAG GAA CGT TTG GAA ATT GCT		204
S L S N Q D H T S K K D P G G H R T A A		612
AGT TTG TCA AAC CAA GAT CAT ACC TCT AAG AAG GAC CCA GGA GGA CAC AGA ACG GCT GCC		224
I L H G G S P D F V G N G K H R A N S S		672
ATT CTA CAT GGA GGC TCT CCT GAC TTT GTA GGA AAT GGT AAA CAT CGG GCA AAC TCC TCA		244
G R S R R E R Q Y S V C N S E D S P G S		732
GGA AGG TCT AGG CGA GAA CGT CAG TAT TCT GTA TGT AAT AGT GAA GAT TCT CCT GGC TCT		264
C E I L Y F N M G S P D Q L M V H K G K		792
TGT GAA ATT CTG TAT TTC AAT ATG GGG AGT CCT GAT CAG CTC ATG GTG CAC AAA GGG AAA		284
C I G S D E Q L G K L V Y N A L E T A T		852
TGT ATT GGC AGT GAT GAA CAA CTT GGA AAA TTA GTC TAC AAT GCT TTG GAA ACA GCC ACT		304
G G F V L L Y E W V L Q W Q K K M G P F		912
GGT GGC TTT GTC TTG TTG TAT GAG TGG GTC CTT CAG TGG CAG AAA AAA ATG GGT CCA TTC		324
L T S Q E K E K I D K C K K Q I Q G T E		972
CTT ACC AGT CAA GAA AAA GAG AAG ATT GAT AAG TGC AAA AAG CAG ATT CAA GGA ACA GAA		344
T E F N S L V K L S H P N V V R Y L A M		1032
ACA GAA TTC AAC TCA CTG GTA AAA TTG AGC CAT CCA AAT GTA GTA CGC TAC CTT GCA ATG		364
N L K E Q D D S I V V D I L V E H I S G		1092
		384

FIG. 1a

AAT CTC AAA GAG CAA GAC GAC TCC TTC GTG GTG GAC ATT TTA GTG GAG CAC ATT AAT GGG 1152
 V S L A A H L S H S G P I P V H Q L R R 404
 GTC TCT CTT GCT GCA CAC CTG AGC CAC TCA GGC CCC ATC CCT GTG CAT CAG CTT CGC AGG 1212
 Y T A Q L L S G L D Y L H S N S V V H K 424
 TAC ACA GCT CAG CTC CTG TCA GGC CTT GAT TAT CTG CAC AGC AAT TCT GTG GTG CAT AAG 1272
 V L S A S N V L V D A E G T V K I T D Y 444
 GTC CTG AGT GCA TCT AAT GTC TTG GTG GAT GCA GAA GGC ACC GTC AAG ATT ACG GAC TAT 1332
 S I S K R L A D I C K E D V F E Q T R V 464
 AGC ATT TCT AAG CGC CTC GCA GAC ATT TGC AAG GAG GAT GTG TTT GAG CAA ACC CGA GTT 1392
 R F S D N A L P Y K T G K K G D V W R L 484
 CGT TTT AGT GAC AAT GCT CTG CCT TAT AAA ACG GGG AAG AAA GGA GAT GTT TGG CGT CTT 1452
 G L L L L S L S Q G Q E C G E Y P V T I 504
 GGC CTT CTG CTG CTG TCC CTC AGC CAA GGA CAG GAA TGT GGA GAG TAC CCT GTG ACC ATC 1512
 P S D L P A D F Q D F L K K C V C L D D 524
 CCT AGT GAC TTA CCA GCT GAC TTT CAA GAT TTT CTA AAG AAA TGT GTG TGC TTG GAT GAC 1572
 K E R W S P Q Q L L K H S F I N P Q P K 544
 AAG GAA AGA TGG AGT CCC CAG CAG TTG TTG AAA CAC AGC TTT ATA AAT CCC CAG CCA AAA 1632
 M P L V E Q S P E D S G G Q D Y V E T V 564
 ATG CCT CTA GTG GAA CAA AGT CCT GAA GAT TCT GGA GGA CAA GAT TAT GTT GAG ACT GTT 1692
 I P S N R L P S A A F F S E T Q R Q F S 584
 ATT CCT AGC AAC CGG CTA CCC AGT GCT GCC TTC TTT AGT GAG ACA CAG AGA CAG TTT TCC 1752
 R Y F I E F E E L Q L L G K G A F G A V 604
 CGA TAC TTC ATT GAG TTT GAA GAA TTA CAA CTT CTT GGT AAA GGA GCT TTT GGA GCT GTC 1812
 I K V Q N K L D G C C Y A V K R I P I N 624
 ATC AAG GTG CAG AAC AAG TTG GAC GGC TGC TGC TAC GCA GTG AAG CGC ATC CCC ATC AAC 1872
 P A S R Q F R R I K G E V T L L S R L H 644
 CCG GCC AGC CGG CAG TTC CGC AGG ATC AAG GGC GAA GTG ACA CTG CTG TCA CGG CTG CAC 1932
 H E N I V R Y Y N A W I E R H E R P A G 664
 CAT GAG AAC ATT GTG CGC TAC TAC AAC GCC TGG ATC GAG CGG CAC GAG CGG CCG GCG GGA 1992
 P G T P P P D S G P L A K D D R A A R G 684
 CCG GGG ACG CCG CCC CCG GAC TCC GGG CCC CTG GCC AAG GAT GAC CGA GCT GCA CGC GGG 2052
 Q P A S D T D G L D S V E A A A P P P I 704
 CAG CCG GCG AGC GAC ACA GAC GGC CTG GAC AGC GTA GAG GCC GCC GCG CCG CCA CCC ATC 2112
 L S S S V E W S T S G E R S A S A R F P 724
 CTC AGC AGC TCG GTG GAG TGG AGC ACT TCG GGC GAG CGC TCG GCC AGT GCC CGT TTC CCC 2172
 A T G P G S S D D E D D D E D E H G G V 744
 GCC ACC GGC CCG GGC TCC AGC GAT GAC GAG GAC GAC GAG GAC GAG CAC GGT GGC GTC 2232
 F S Q S F L P A S D S E S D I I F D N E 764
 TTC TCC CAG TCC TTC CTG CCT GCT TCA GAT TCT GAA AGT GAT ATT ATC TTT GAC AAT GAA 2292
 D E N S K S Q N Q D E D C N E K N G C H 784
 GAT GAG AAC AGT AAA AGT CAG AAT CAG GAT GAA GAT TGC AAT GAA AAG AAT GGC TGC CAT 2352

FIG. 1b

E S E P S V T T E A V H Y L Y I Q M E Y 804
 GAA AGT GAG CCA TCA GTG ACG ACT GAG GCT GTG CAC TAC CTA TAC ATC CAG ATG GAG TAC 2412
 C E K S T L R D T I D Q G L Y R D T V R 824
 TGT GAG AAG AGC ACT TTA CGA GAC ACC ATT GAC CAG GGA CTG TAT CGA GAC ACC GTC AGA 2472
 L W R L F R E I L D G L A Y I H E K G M 844
 CTC TGG AGG CTT TTT CGA GAG ATT CTG GAT GGA TTA GCT TAT ATC CAT GAG AAA GGA ATG 2532
 I H R D L K P V N I F L D S D D H V K I 864
 ATT CAC CGG GAT TTG AAG CCT GTC AAC ATT TTT TTG GAT TCT GAT GAC CAT GTG AAA ATA 2592
 G D F G L A T D H L A F S A D S K Q D D 884
 GGT GAT TTT GGT TTG GCG ACA GAC CAT CTA GCC TTT TCT GCT GAC AGC AAA CAA GAC GAT 2652
 Q T G D L I K S D P S G H L T G M V G T 904
 CAG ACA GGA GAC TTG ATT AAG TCA GAC CCT TCA GGT CAC TTA ACT GGG ATG GTT GGC ACT 2712
 A L Y V S P E V Q G S T K S A Y N Q K V 924
 GCT CTC TAT GTA AGC CCA GAG GTC CAA GGA AGC ACC AAA TCT GCA TAC AAC CAG AAA GTG 2772
 D L F S L G I I F F E M S Y H P M V T A 944
 GAT CTC TTC AGC CTG GGA ATT ATC TTC TTT GAG ATG TCC TAT CAC CCC ATG GTC ACG GCT 2832
 S E R I F V L N Q L R D P T S P K F P E 964
 TCA GAA AGG ATC TTT GTT CTC AAC CAA CTC AGA GAT CCC ACT TCG CCT AAG TTT CCA GAA 2892
 D F D D G E H A K Q K S V I S W L L N H 984
 GAC TTT GAC GAT GGA GAG CAT GCA AAG CAG AAA TCA GTC ATC TCC TGG CTG TTG AAC CAC 2952
 D P A K R P T A T E L L K S E L L P P P 1004
 GAT CCA GCA AAA CGG CCC ACA GCC ACA GAA CTG CTC AAG AGT GAG CTG CTG CCC CCA CCC 3012
 Q M E E S E L H E V L H H T L T N V D G 1024
 CAG ATG GAG GAG TCA GAG CTG CAT GAA GTG CTG CAC CAC ACG CTG ACC AAC GTG GAT GGG 3072
 K A Y R T M M A Q I F S Q R I S P A I D 1044
 AAG GCC TAC CGC ACC ATG ATG GCC CAG ATC TTC TCG CAG CGC ATC TCC CCT GCC ATC GAT 3132
 Y T Y D S D I L K G N F S I R T A K M Q 1064
 TAC ACC TAT GAC AGC GAC ATA CTG AAG GGC AAC TTC TCA ATC CGT ACA GCC AAG ATG CAG 3192
 Q H V C E T I I R I F K R H G A V Q L C 1084
 CAG CAT GTG TGT GAA ACC ATC ATC CGC ATC TTT AAA AGA CAT GGA GCT GTT CAG TTG TGT 3252
 T P L L L P R N R Q I Y E H N E A A L F 1104
 ACT CCA CTA CTG CTT CCC CGA AAC AGA CAA ATA TAT GAG CAC AAC GAA GCT GCC CTA TTC 3312
 M D H S G M L V M L P F D L R I P F A R 1124
 ATG GAC CAC AGC GGG ATG CTG GTG ATG CTT CCT TTT GAC CTG CGG ATC CCT TTT GCA AGA 3372
 Y V A R N N I L N L K R Y C I E R V F R 1144
 TAT GTG GCA AGA AAT AAT ATA TTG AAT TTA AAA CGA TAC TGC ATA GAA CGT GTG TTC AGG 3432
 P R K L D R F H P K E L L E C A F D I V 1164
 CCG CGC AAG TTA GAT CGA TTT CAT CCC AAA GAA CTT CTG GAG TGT GCA TTT GAT ATT GTC 3492
 T S T T N S F L P T A E I I Y T I Y E I 1184
 ACT TCT ACC ACC AAC AGC TTT CTG CCC ACT GCT GAA ATT ATC TAC ACT ATC TAT GAA ATC 3552

FIG. 1c

I Q E F P A L Q E R N Y S I Y L N H I M	1204
ATC CAA GAG TTT CCA GCA CTT CAG GAA AGA AAT TAC AGT ATT TAT TTG AAC CAT ACC ATG	3612
L L K A I L L H C G I P E D K L S Q V Y	1224
TTA TTG AAA GCA ATA CTC TTA CAC TGT GGG ATC CCA GAA GAT AAA CTC AGT CAA GTC TAC	3672
I I L Y D A V T E K L T R R E V E A K F	1244
ATT ATT CTG TAT GAT GCT GTG ACA GAG AAG CTG ACG AGG AGA GAA GTG GAA GCT AAA TTT	3732
C N L S L S S N S L C R L Y K F I E Q K	1264
TGT AAT CTG TCT TTG TCT TCT AAT AGT CTG TGT CGA CTC TAC AAG TTT ATT GAA CAG AAG	3792
G D L Q D L M P T I N S L I K Q K T G I	1284
GGA GAT TTG CAA GAT CTT ATG CCA ACA ATA AAT TCA TTA ATA AAA CAG AAA ACA GGT ATT	3852
A Q L V K Y G L K D L E E V V G L L K K	1304
GCA CAG TTG GTG AAG TAT GGC TTA AAA GAC CTA GAG GAG GTT GTT GGA CTG TTG AAG AAA	3912
L G I K L Q V L I N L G L V Y K V Q Q H	1324
CTC GGC ATC AAG TTA CAG GTC TTG ATC AAT TTG GGC TTG GTT TAC AAG GTG CAG CAG CAC	3972
N G I I F Q F V A F I K R R Q R A V P E	1344
AAT GGA ATC ATC TTC CAG TTT GTG GCT TTC ATC AAA CGA AGG CAA AGG GCT GTA CCT GAA	4032
I L A A G G R Y D L L I P Q F R G P Q A	1364
ATC CTC GCA GCT GGA GGC AGA TAT GAC CTG CTG ATT CCC CAG TTT AGA GGG CCA CAA GCT	4092
L G P V P T A I G V S I A I D K I S A A	1384
CTG GGG CCA GTT CCC ACT GCC ATT GGG GTC AGC ATA GCT ATA GAC AAG ATA TCT GCT GCT	4152
V L N M E E S V T I S S C D L L V V S V	1404
CTC CTC AAC ATG GAG GAA TCT GTT ACA ATA AGC TCT TGT GAC CTC CTG GTT GTA AGT GTT	4212
G Q M S M S R A I N L T Q K L W T A G I	1424
GGT CAG ATG TCT ATG TCC AGG GCC ATC AAC CTA ACC CAG AAA CTC TGG ACA GCA GGC ATC	4272
T A E I M Y D W S Q S Q E E L Q E Y C R	1444
ACA GCA GAA ATC ATG TAC GAC TGG TCA CAG TCC CAA GAG GAA TTA CAA GAG TAC TGC AGA	4332
H H E I T Y V A L V S D K E G S H V K V	1464
GAT CAT GAA ATC ACC TAT GTG GCC CTT GTC TCG GAT AAA GAA GGA AGC CAT GTC AAG GTT	4392
K S F E K E R Q T E K R V L E T E L V D	1484
AAG TCT TTC GAG AAG GAA AGG CAG ACA GAG AAG CGT GTG CTG GAG ACT GAA CTT GTG GAC	4452
H V L Q K L R T K V T D E R N G R E A S	1504
CAT GTA CTG CAG AAA CTG AGG ACT AAA GTC ACT GAT GAA AGG AAT GGC AGA GAA GCT TCC	4512
D N L A V Q N L K G S F S N A S G L F E	1524
GAT AAT CTT GCA GTG CAA AAT CTG AAG GGG TCA TTT TCT AAT GCT TCA GGT TTG TTT GAA	4572
I H G A T V V P I V S V L A P E K L S A	1544
ATC CAT GGA GCA ACA GTG GTT CCC ATT GTG AGT GTG CTA GCC CCG GAG AAG CTG TCA GCC	4632
S T R R R Y E T Q V Q T R L Q T S L A N	1564
AGC ACT AGG AGG CGC TAT GAA ACT CAG GTA CAA ACT CGA CTT CAG ACC TCC CTT GCC AAC	4692
L H Q K S S E I E I L A V D L P K E T I	1584
TTA CAT CAG AAA AGC AGT GAA ATT GAA ATT CTG GCT GTG GAT CTA CCC AAA GAA ACA ATA	4752
L Q F L S L E W D A D E Q A F N T T V K	1604

FIG. 1d

TTA CAG TTT TTA TCA TTA GAG TGG GAT GCT GAT GAA CAG GCA TTT AAC ACA ACT GTG AAG 4812
 Q L L S R L P K Q R Y L K L V C D E I Y 1624
 CAG CTG CTG TCA CGC CTG CCA AAG CAA AGA TAC CTC AAA TTA GTC TGT GAT GAA ATT TAT 4872
 N I K V E K K V S V L F L Y S Y R D D Y 1644
 AAC ATC AAA GTA GAA AAA AAG GTG TCT GTG CTA TTT CTG TAC AGC TAT AGA GAT GAC TAC 4932
 Y R I L F * 1650
 TAC AGA ATC TTA TTT TAA 4950

CCCTAAAGAACTGTCGTTAACCTCATTTCAAACAGACAGAGGCTTATACTGGAATAATGGAATGTTGTACATTCATCATA
 ATTTAAATTTAAATTTCTAAGAAGAGGCTGGGTGCAGTGGCTCACACCTTTAATCCCAGCACTTTGGGAAGCCAAGGCAG
 GAAGACTGCTTGAAACCAGGAGTTTGAGACCAGCCTGAGCAACAAAGCAAGACCCCATCTCTATAAAAACTAAAAAAT
 TAGTTGGGCATGGTGGCACATGCCTGTAGTCCCAGCTACTCCAGAGGCTGAGATGGATCATCTGAGCCTCAGGAGGTTG
 AGGCTGCAGTGAGCTGTGACTGCGCCACTGCACTCCAGTCTGGGACAACAGAGCAAGACCCCTGTCTTAAAAAAAAAAG
 AAAAAAAAAATTTTTTCTAAGAAGCTGTCCTACAAAGTTGAGCTTTGTTAGTTTTCATGTGTAATATATTATAAATT
 TATCTTTTGGGATATAATAAATGCTTTCATATACCTGCA

006220-90851560

FIG. 1e

CLUSTAL W (1.74) multiple sequence alignment

6065914_eIF2kinase_man 14790	----- MAGGRGAPGRGRDEPPESYPQRQDHELQALEAIYGADFQDLRPDACPVK
6066585_eIF2kinase_mouse	MAGGRGASGRGRAEPQESYSQRQDHELQALEAIYGSDFDLDPDARGVR
6065914_eIF2kinase_man 14790	----- EPPEINLVLPQGLTGEEVYVKVDLRVKCPPTYPDVVPEIELKNAKGLSN
6066585_eIF2kinase_mouse	EPPEINLVLPQGLAGEEVYVQVELQVKCPPTYPDVVPEIELKNAKGLSN
6065914_eIF2kinase_man 14790	----- ESVNLLKSRLEELAKKHCGEVMIFELAYHVQSFLSEHNKPPPKSFHEEML
6066585_eIF2kinase_mouse	ESVNLLKSHLEELAKKQCCEVMIFELAHVQSFLSEHNKPPPKSFHEEML
6065914_eIF2kinase_man 14790	----- ERRAQEEQORLLEAKRKEEQEQREILHEIQRRKEEIKEEKKRKEMAKQER
6066585_eIF2kinase_mouse	ERQAQEKQORLLEARRKEEQEQREILHEIQRRKEEIKEEKKRKEMAKQER
6065914_eIF2kinase_man 14790	----- LEIASLSNQDHTSKKDPGGHRTAAILHGGSPDFVGNKGHRANSRSGRSRRE
6066585_eIF2kinase_mouse	LEITSLTNQDYASKRDPAGHRAAAILHGGSPDFVGNKGARTYSSGRSRRE
6065914_eIF2kinase_man 14790	----- RQYSVCNSEDSPGSCIEILYFNMGSPDQLMVHKGKICGSDEQLGKLVYNAL
6066585_eIF2kinase_mouse	RQYSVCSGEPSPGSCDILHFSVGSPPDQLMVHKGRCVGSDEQLGKVYNAL
6065914_eIF2kinase_man 14790	----- ETATGGFVLLYEWVLQWQKMGPFLLTSQEKEKIDKCKKQIQGTETEFNSL
6066585_eIF2kinase_mouse	ETATGSFVLLHEWVLQWQK-MGPCLTSQEKEKIDKCKRQIQGAETEFSSL
6065914_eIF2kinase_man 14790	----- VKLSHPNVVRYLAMNLKEQDDSIIVVDILVEHISGVSLAAHLSHSGPIPVH
6066585_eIF2kinase_mouse	VKLSHPNIVRYFAMNSREEEDSIVIDILAEHVSGISLATHLSHSGPVPAP
6065914_eIF2kinase_man 14790	----- QLRRYTAQLLSGLDYLHSNSVVKVLSASNVLVDAEGTVKITDYSISKRL
6066585_eIF2kinase_mouse	QLRKYTAQLLAGLDYLHSNSVVKVLSASSVLVDAEGTVKITDYSISKRL
6065914_eIF2kinase_man 14790	----- ADICKEDVFEQTRVRFSDNALPYKTGKKGDVWRLGLLLLSLSQGQECGEY
6066585_eIF2kinase_mouse	ADICKEDVFEQARVRFSDSALPYKTGKKGDVWRLGLLLLSLSQGQECGEY
6065914_eIF2kinase_man 14790	----- PVTIPSDLPADFQDFLKKCVCLDDKERWSPQQLLKHSFINPQPKMPLVEQ
6066585_eIF2kinase_mouse	PVTIPSDLPADFQDFLKKCVCLDDKERWSPQQLLKHSFINPQPKLPLVEQ
6065914_eIF2kinase_man 14790	----- SPEDSGGQDYVETVIPSRLPSAAFFSETQRQFSRYFIEFEELQLLGKGA
6066585_eIF2kinase_mouse	SPEDSGGQDYIETVIPSRLPSAAFFSETQKQFSRYFIEFEELQLLGKGA
6065914_eIF2kinase_man 14790	----- FGAVIKVQNKLDGCCYAVKRIPINPASRQFRRIKGEVTLLSRLHHENIVR
6066585_eIF2kinase_mouse	FGAVIKVQNKLDGCCYAVKRIPINPASRHFRIKGEVTLLSRLHHENIVR
6065914_eIF2kinase_man 14790	----- YYNAWIERHERPAGPGTPPPDSGLAKDDRAARGQPASDTDGLDSVEAAA
6066585_eIF2kinase_mouse	YYNAWIERHERPAVPGTPPPDCTPQAQDSPATCGKTSKDTEELGSVEAAA

FIG. 2a

6065914_eIF2kinase_man 14790 6066585_eIF2kinase_mouse	----- PPPISSSSVWSTSGERSASARFPATGPGSSDDEDDDEHGGVFSQSFL PPPISSSSVWSTSAERSTSTRFPVTGQDSSSDEED-EDERDGVFSQSFL
6065914_eIF2kinase_man 14790 6066585_eIF2kinase_mouse	----- PASDSESDIIFDNEDENSKSQNQDEDCNEKNGCHESEPSVTTEAVHYLYI PASDSDSDIIFDNEDENSKSQNQDEDCNQKDGSHIEPSVTAEAVHYLYI
6065914_eIF2kinase_man 14790 6066585_eIF2kinase_mouse	----- QMEYCEKSTLRDTIDQGLYRDTVRLWRLFREILDGLAYIHEKGMHRDLK QMEYCEKSTLRDTIDQGLFRDTSRLWRLFREILDGLAYIHEKGMHRDLK
6065914_eIF2kinase_man 14790 6066585_eIF2kinase_mouse	----- PVNIFLSDSDHVKIGDFGLATDHLAFSADSKQDDQTGD-LIKSDPSGHLT PVNIFLSDSDHVKIGDFGLATDHLAFTAEGKQDDQAGDGVIKSDPSGHLT
6065914_eIF2kinase_man 14790 6066585_eIF2kinase_mouse	----- GMVGTALYVSPEVQGSTKSAYNQKVDLFSLGIIFFEMSYHPMTASERIF GMVGTALYVSPEVQGSTKSAYNQKVDLFSLGIIFFEMSYHPMTASERIF
6065914_eIF2kinase_man 14790 6066585_eIF2kinase_mouse	----- VLNQLRDPTSPKFPEDFDDGEHAKQKSVISWLLNHDPKRPTATELLKSE VLNQLRDPTSPKFPDDFDDGEHTKQKSVISWLLNHDPKRPTAMELLKSE
6065914_eIF2kinase_man 14790 6066585_eIF2kinase_mouse	----- LLPPPQMEESSELHEVLHHTLTNVDGKAYRTMMAQIFSQRISPAIDYTYDS LLPPPQMEESSELHEVLHHTLANIDGKAYRTMMSQIFCOHISPAIDYTYDS
6065914_eIF2kinase_man 14790 6066585_eIF2kinase_mouse	----- DILKGNFSIRTAKMQQHVCETIIRIFKRHGAVQLCTPLLLPRNRQIYEHN DILKGNFLIRTAKIQQLVCETIVRVFKRHGAVQLCTPLLLPRNRQIYEHN
6065914_eIF2kinase_man 14790 6066585_eIF2kinase_mouse	----- --ALFMDHSGMLVMLPFDLRIPFARYVARNNILILKRYCIERVFRPRKLD EAALFMDHSGMLVMLPFDLRIPFARYVARNNILNLKRYCIERVFRPRKLD EAALFMDHSGMLVMLPFDLRVPFARYVARNNILNLKRYCIERVFRPRKLD *****:*****
6065914_eIF2kinase_man 14790 6066585_eIF2kinase_mouse	----- RFHPKELLECAFDIVTSTTNSFLPTAEIIYTIYEIIQEFPALQERNYSIY RFHPKELLECAFDIVTSTTNSFLPTAEIIYTIYEIIQEFPALQERNYSIY RFHPKELLECAFDIVTSTTNSLPTAETIYTIYEIIQEFPALQERNYSIY *****:*****
6065914_eIF2kinase_man 14790 6066585_eIF2kinase_mouse	----- LNHTMLLKAILLHCGIPEDKLSQVYIILYDAVTEKLTRREVEAKFCNLSL LNHTMLLKAILLHCGIPEDKLSQVYIILYDAVTEKLTRREVEAKFCNLSL LNHTMLLKAILLHCGIPEDKLSQVYIILYDAVTEKLTRREVEAKFCNLSL *****:*****
6065914_eIF2kinase_man 14790 6066585_eIF2kinase_mouse	----- SSNSLCRLYKFIEQKGLQDLMPTINSLIKQKTGIAQLVKYGLKDLEEVV SSNSLCRLYKFIEQKGLQDLMPTINSLIKQKTGIAQLVKYGLKDLEEVV SSNSLCRLYKFIEQKGLQDLTPPTINSLIKQKTGVAQLVKYSLKDLEDVV *****:*****:*****:*****:*****
6065914_eIF2kinase_man 14790 6066585_eIF2kinase_mouse	----- GLLKKLGIKLQVLINLGLVYKVQQHNGIIFQFVAFIKRRQRAVPEILAAG GLLKKLGIKLQVLINLGLVYKVQQHNGIIFQFVAFIKRRQRAVPEILAAG GLLKKLGVLQVLSINLGLVYKVQQHTGIIFQFLAFSKRRQRVPEILAAG *****:*****:*****:*****:*****
6065914_eIF2kinase_man 14790 6066585_eIF2kinase_mouse	----- GRYDLLIPQFRGPQALGPVPTAIGVSAIDKISAAVLNMEESVTISSCDL GRYDLLIPQFRGPQALGPVPTAIGVSAIDKISAAVLNMEESVTISSCDL GRYDLLIPKFRGPQTVGPVPTAVGVSAIDKIFAVVLNMEEPVTVSSCDL *****:*****:*****:*****:*****
6065914_eIF2kinase_man	----- LVVSVGQMSMSRAINLTQKLWTAGITAEIMYDWSQSQEELQEYCRHHEIT

FIG. 2b

14790
6066585_eIF2kinase_mouse

LVVSVQMSMSRAINLTQKLWTAGITAEIMYDWSQSQEELQEYCRHHEIT
LVVSVGQMSMSRAINLTQKLWTAGITAEIMYDWSQSQEELQEYCRHHEIT

6065914_eIF2kinase_man
14790
6066585_eIF2kinase_mouse

YVALVSDKEGSHVKVKSFEKERQTEKRVLETELVDHVLQKLRTKVTDERN
YVALVSDKEGSHVKVKSFEKERQTEKRVLETELVDHVLQKLRTKVTDERN
YVALVSDKEGSHVKVKSFEKERQTEKRVLESDLDHVMQKLRTKVGDERN
*****:*****

6065914_eIF2kinase_man
14790
6066585_eIF2kinase_mouse

GREASDNLAVQNLKGSFSNASGLFEIHGATVVPIVSVLAPEKLSASTRRR
GREASDNLAVQNLKGSFSNASGLFEIHGATVVPIVSVLAPEKLSASTRRR
FRDASDNLAVQTLKGSFSNASGLFEIHGTTPVVPNVIVLAPEKLSASTRRR
*:*****

6065914_eIF2kinase_man
14790
6066585_eIF2kinase_mouse

YETQVQTRLQTSANLHQKSSEIEILAVDLPKETILQFLSLEWDADEQAF
YETQVQTRLQTSANLHQKSSEIEILAVDLPKETILQFLSLEWDADEQAF
HEIQVQTRLQTTLANLHQKSSEIEILAVDLPKETILQFLSLEWDADEQAF
:* *****

6065914_eIF2kinase_man
14790
6066585_eIF2kinase_mouse

NTTVKQLLSRLPKQRYLKLVCDEIYNIKVEKKVSVLFLYSYRDDYYRILF
NTTVKQLLSRLPKQRYLKLVCDEIYNIKVEKKVSVLFLYSYRDDYYRILF
NTTVKQLLSRLPKQRYLKLVCDEIYNIKVEKKVSVLFLYSYRDDYYRILF

006220"90251550

FIG. 2c